

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/529,349A  
Source: IFWP  
Date Processed by STIC: 8/4/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 08/04/2006

PATENT APPLICATION: US/10/529,349A

TIME: 12:13:51

Input Set : E:\P1988R1 Sequence Listing.txt

Output Set: N:\CRF4\08042006\J529349A.raw

3 <110> APPLICANT: Bodary-Winter, Sarah C.  
 4 Clark, Hilary  
 5 Jackman, Janet K.  
 6 Schoenfeld, Jill R.  
 7 Williams, P. Mickey  
 8 Wood, William I.  
 9 Wu, Thomas D.

11 <120> TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of Psoriasis

13 <130> FILE REFERENCE: P1988R1-US  
 15 <140> CURRENT APPLICATION NUMBER: US 10/529,349A  
 16 <141> CURRENT FILING DATE: 2005-03-25  
 18 <150> PRIOR APPLICATION NUMBER: PCT/US03/027382  
 19 <151> PRIOR FILING DATE: 2003-08-28  
 21 <150> PRIOR APPLICATION NUMBER: US 60/414,484  
 22 <151> PRIOR FILING DATE: 2002-09-26  
 24 <160> NUMBER OF SEQ ID NOS: 48  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 3192  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Homo sapiens  
 31 <400> SEQUENCE: 1

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 36 cccatactca gtagccacga tggagggtgat gaacctgatg gagcagccta 150  
 38 tcaagggtgac tgagtgccag cagacataca cctacgactc gggatatccac 200  
 40 tcgggcgcga acacctgcgt gccctccgtc agcagcaagg gcatcatgga 250  
 42 ggaggatgag gcctgccccg gccagtagac gctcaagaaa accaccactt 300  
 44 acaccagggg ggtgcccccc agccaagggtg acctggagta ccagatgtcc 350  
 46 acaacagcca gggccaaacg ggtgcggggag gccatgtgcc ctggtgtgtc 400  
 48 aggcgaggac agctcgcttc tgctggccac ccagggtggag gggcaggcca 450  
 50 ccaacctgca gcgactggcc gagccgtccc agctgctcaa gtcggccatt 500  
 52 gtgcatctca tcaactacca ggacgatgcc gagctggcca ctgcgcacct 550  
 54 gcccgagctc accaaactgc tcaacgacga ggaccgggtg gtggtgacca 600  
 56 aggcggccat gattgtgaac cagctgtcga agaaggaggc gtcgcggcgg 650  
 58 gccctgatgg gctcgcccca gctgggtggc gctgtcgtgc gtaccatgca 700  
 60 gaataccagc gacctggaca cagcccgcgt caccaccagc atcctgcaca 750  
 62 acctctccca ccaccgggag gggctgctcg ccatcttcaa gtcgggtggc 800  
 64 atccctgctc tggtcgcgat gctcagctcc cctgtggagt cggtcctgtt 850  
 66 ctatgccatc accacgtgc acaacctgct cctgtaccag gagggcgcca 900  
 68 agatggccgt gcgcctggcc gacgggctgc aaaagatggt gcccctgctc 950  
 70 aacaagaaca accccaagtt cctggccatc accaccgact gcctgcagct 1000  
 72 cctggcctac ggcaaccagg agagcaagct gatcatcctg gccaatggtg 1050  
 74 ggccccaggc cctcgtgcag atcatgcgta actacagtta tgaaaagctg 1100

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80 tgaccagcaa cagccccgcg ctggtgcaga actgcctgtg gaccctgcgc 1250
82 aacctctcag atgtggccac caagcaggag ggcttgaga gtgtgctgaa 1300
84 gattctggtg aatcagctga gtgtggatga cgtcaacgtc ctcacctgtg 1350
86 ccacggggcac actctccaac ctgacatgca acaacagcaa gaacaagacg 1400
88 ctggtgacac agaacagcgg tgtggaggct ctcatccatg ccacctgcg 1450
90 tgctggtgac aaggacgaca tcacggagcc tgccgtctgc gctctgcgcc 1500
92 acctactag ccgccaccct gagggcgaga tggcccagaa ctctgtgcgt 1550
94 ctcaactatg gcatcccagc catcgtgaag ctgctcaacc agcccaacca 1600
96 gtggccactg gtcaaggcaa ccacggctt gatcaggaat ctggccctgt 1650
98 gcccagccaa ccatgccccg ctgcaggagg cagcggctcat ccccgccctc 1700
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104 agggctgcac cggagcactg cacatcctcg cccgggaccc catgaaccgc 1850
106 atggagatct tccggctcaa caccattccc ctgtttgtgc agctcctgta 1900
108 ctctgcgggt gagaacatcc agcgcgtggc tgccgggggtg ctgtgtgagc 1950
110 tggccctagga caaggaggcg gccgacgcca ttgatgcaga gggggcctcg 2000
112 gcccactca tggagtgtct gcactccgc aacgagggca ctgccacctc 2050
114 cgctgctgcc gtctgttcc gcatctccga ggacaagaac ccagactacc 2100
116 ggaagcgcgt gtccgtggag ctcaccaact cctcttcaa gcatgaccgc 2150
118 gctgcctggg aggtgccc gagcatgatt cccatcaatg agccctatgg 2200
120 agatgacatg gatgccacct accgccccat gtactccagc gatgtgcccc 2250
122 ttgaccgct ggagatgcac atggacatgg atggagacta ccccatcgac 2300
124 acctacagcg acggcctcag gccccgtac cccactgcag accacatgct 2350
126 ggcctaggcg gcctggcccc agtgcggttc ctcatctgag aggctctccg 2400
128 tgcaggcgat ggggcaagac agaaaagtgc ctgagctggg gaagccgggg 2450
130 tgtaacttcc tgctgcaccc tgcgcctcca gaggtcctcc gtagggctct 2500
132 tcttgggata gtgttctgct cctgcttttc tgcctgggc atgggtccag 2550
134 ggcctgacac cccctccccg cccctgtggc cctggccact aaagcttcag 2600
136 actcaagtac ccattctgtt tccccccagc aacgcccctc caaacctcca 2650
138 gcctccctgt ctccagctgc ctgggcccgg aagggtttg gttccttctc 2700
140 tgggtctgat tttctcactg aactccaccg accaactgcc ctaagcccc 2750
142 agggcctcca gggcccagggt tgcgagacca aacccccaaa atccaaaact 2800
144 tctcttgaaa agttcaggga ccgtccaggg gagatgggga ggagatatgg 2850
146 agtgagtcac ctgctccaga agatgccagc ttctctctcc aggggtgctta 2900
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150 tcacaccct gtcccacca cacagctgcc ctactgacc ccgagaagtg 3000
152 ctcttggtg acccctctgg tgtgtggtga ggggctttct cttcccttcc 3050
154 ctgtttcaga cccccccatt tccgcacat ggtgtggggg gctgggggag 3100
156 gtccaagcag agtggtttat tattatcgct ttatgtttt gggtattggg 3150
158 tttttgtat agaccaaagc aaagaaaata aaaataacac ag 3192
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 745
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 2
166 Met Glu Val Met Asn Leu Met Glu Gln Pro Ile Lys Val Thr Glu
167 1 5 10 15

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169	Trp	Gln	Gln	Thr	Tyr	Thr	Tyr	Asp	Ser	Gly	Ile	His	Ser	Gly	Ala
170					20					25					30
172	Asn	Thr	Cys	Val	Pro	Ser	Val	Ser	Ser	Lys	Gly	Ile	Met	Glu	Glu
173					35					40					45
175	Asp	Glu	Ala	Cys	Gly	Arg	Gln	Tyr	Thr	Leu	Lys	Lys	Thr	Thr	Thr
176					50					55					60
178	Tyr	Thr	Gln	Gly	Val	Pro	Pro	Ser	Gln	Gly	Asp	Leu	Glu	Tyr	Gln
179					65					70					75
181	Met	Ser	Thr	Thr	Ala	Arg	Ala	Lys	Arg	Val	Arg	Glu	Ala	Met	Cys
182					80					85					90
184	Pro	Gly	Val	Ser	Gly	Glu	Asp	Ser	Ser	Leu	Leu	Leu	Ala	Thr	Gln
185					95					100					105
187	Val	Glu	Gly	Gln	Ala	Thr	Asn	Leu	Gln	Arg	Leu	Ala	Glu	Pro	Ser
188					110					115					120
190	Gln	Leu	Leu	Lys	Ser	Ala	Ile	Val	His	Leu	Ile	Asn	Tyr	Gln	Asp
191					125					130					135
193	Asp	Ala	Glu	Leu	Ala	Thr	Arg	Ala	Leu	Pro	Glu	Leu	Thr	Lys	Leu
194					140					145					150
196	Leu	Asn	Asp	Glu	Asp	Pro	Val	Val	Val	Thr	Lys	Ala	Ala	Met	Ile
197					155					160					165
199	Val	Asn	Gln	Leu	Ser	Lys	Lys	Glu	Ala	Ser	Arg	Arg	Ala	Leu	Met
200					170					175					180
202	Gly	Ser	Pro	Gln	Leu	Val	Ala	Ala	Val	Val	Arg	Thr	Met	Gln	Asn
203					185					190					195
205	Thr	Ser	Asp	Leu	Asp	Thr	Ala	Arg	Cys	Thr	Thr	Ser	Ile	Leu	His
206					200					205					210
208	Asn	Leu	Ser	His	His	Arg	Glu	Gly	Leu	Leu	Ala	Ile	Phe	Lys	Ser
209					215					220					225
211	Gly	Gly	Ile	Pro	Ala	Leu	Val	Arg	Met	Leu	Ser	Ser	Pro	Val	Glu
212					230					235					240
214	Ser	Val	Leu	Phe	Tyr	Ala	Ile	Thr	Thr	Leu	His	Asn	Leu	Leu	Leu
215					245					250					255
217	Tyr	Gln	Glu	Gly	Ala	Lys	Met	Ala	Val	Arg	Leu	Ala	Asp	Gly	Leu
218					260					265					270
220	Gln	Lys	Met	Val	Pro	Leu	Leu	Asn	Lys	Asn	Asn	Pro	Lys	Phe	Leu
221					275					280					285
223	Ala	Ile	Thr	Thr	Asp	Cys	Leu	Gln	Leu	Leu	Ala	Tyr	Gly	Asn	Gln
224					290					295					300
226	Glu	Ser	Lys	Leu	Ile	Ile	Leu	Ala	Asn	Gly	Gly	Pro	Gln	Ala	Leu
227					305					310					315
229	Val	Gln	Ile	Met	Arg	Asn	Tyr	Ser	Tyr	Glu	Lys	Leu	Leu	Trp	Thr
230					320					325					330
232	Thr	Ser	Arg	Val	Leu	Lys	Val	Leu	Ser	Val	Cys	Pro	Ser	Asn	Lys
233					335					340					345
235	Pro	Ala	Ile	Val	Glu	Ala	Gly	Gly	Met	Gln	Ala	Leu	Gly	Lys	His
236					350					355					360
238	Leu	Thr	Ser	Asn	Ser	Pro	Arg	Leu	Val	Gln	Asn	Cys	Leu	Trp	Thr
239					365					370					375
241	Leu	Arg	Asn	Leu	Ser	Asp	Val	Ala	Thr	Lys	Gln	Glu	Gly	Leu	Glu

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242		380		385		390
244	Ser Val Leu Lys	Ile Leu Val Asn Gln	Leu Ser Val Asp Asp	Val		
245		395		400		405
247	Asn Val Leu Thr	Cys Ala Thr Gly Thr	Leu Ser Asn Leu Thr	Cys		
248		410		415		420
250	Asn Asn Ser Lys	Asn Lys Thr Leu Val	Thr Gln Asn Ser Gly	Val		
251		425		430		435
253	Glu Ala Leu Ile	His Ala Ile Leu Arg	Ala Gly Asp Lys Asp	Asp		
254		440		445		450
256	Ile Thr Glu Pro	Ala Val Cys Ala Leu	Arg His Leu Thr Ser	Arg		
257		455		460		465
259	His Pro Glu Ala	Glu Met Ala Gln Asn	Ser Val Arg Leu Asn	Tyr		
260		470		475		480
262	Gly Ile Pro Ala	Ile Val Lys Leu Leu	Asn Gln Pro Asn Gln	Trp		
263		485		490		495
265	Pro Leu Val Lys	Ala Thr Ile Gly Leu	Ile Arg Asn Leu Ala	Leu		
266		500		505		510
268	Cys Pro Ala Asn	His Ala Pro Leu Gln	Glu Ala Ala Val Ile	Pro		
269		515		520		525
271	Arg Leu Val Gln	Leu Leu Val Lys Ala	His Gln Asp Ala Gln	Arg		
272		530		535		540
274	His Val Ala Ala	Gly Thr Gln Gln Pro	Tyr Thr Asp Gly Val	Arg		
275		545		550		555
277	Met Glu Glu Ile	Val Glu Gly Cys Thr	Gly Ala Leu His Ile	Leu		
278		560		565		570
280	Ala Arg Asp Pro	Met Asn Arg Met Glu	Ile Phe Arg Leu Asn	Thr		
281		575		580		585
283	Ile Pro Leu Phe	Val Gln Leu Leu Tyr	Ser Ser Val Glu Asn	Ile		
284		590		595		600
286	Gln Arg Val Ala	Ala Gly Val Leu Cys	Glu Leu Ala Gln Asp	Lys		
287		605		610		615
289	Glu Ala Ala Asp	Ala Ile Asp Ala Glu	Gly Ala Ser Ala Pro	Leu		
290		620		625		630
292	Met Glu Leu Leu	His Ser Arg Asn Glu	Gly Thr Ala Thr Tyr	Ala		
293		635		640		645
295	Ala Ala Val Leu	Phe Arg Ile Ser Glu	Asp Lys Asn Pro Asp	Tyr		
296		650		655		660
298	Arg Lys Arg Val	Ser Val Glu Leu Thr	Asn Ser Leu Phe Lys	His		
299		665		670		675
301	Asp Pro Ala Ala	Trp Glu Ala Ala Gln	Ser Met Ile Pro Ile	Asn		
302		680		685		690
304	Glu Pro Tyr Gly	Asp Asp Met Asp Ala	Thr Tyr Arg Pro Met	Tyr		
305		695		700		705
307	Ser Ser Asp Val	Pro Leu Asp Pro Leu	Glu Met His Met Asp	Met		
308		710		715		720
310	Asp Gly Asp Tyr	Pro Ile Asp Thr Tyr	Ser Asp Gly Leu Arg	Pro		
311		725		730		735
313	Pro Tyr Pro Thr	Ala Asp His Met Leu	Ala			
314		740		745		

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316 <210> SEQ ID NO: 3
317 <211> LENGTH: 1120
318 <212> TYPE: DNA
319 <213> ORGANISM: Homo sapiens
321 <400> SEQUENCE: 3
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324 caagcgggcc aaagccaagg ccaccaagaa gcggccacag cgggccacat 100
326 ccaatgtctt cgcaatgttt gaccagtccc agatccagga gttaaggag 150
328 gctttcaaca tgattgacca gaaccgtgat ggcttcattg acaaggagga 200
330 cctgcacgac atgctggcct cgctggggaa gaacccaca gacgaatacc 250
332 tggagggcat gatgagcgag gcccgggggc catacaactt caccatgttc 300
334 ctcaccatgt ttggggagaa gctgaacggc acggaccccg aggatgtgat 350
336 tcgcaacgcc ttgacctgct tcgacgagga atcctcaggt ttcacccatg 400
338 aggaccacct ccggaagctg ctcaccacca tgggtgaccg cttcacagat 450
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356 tccggggctg ttccccgagg aggaagggaa gcctctgtgt gccccccagg 900
358 aggaagaggc cctgagtcct gggatcagac accccttcac gtgtatccca 950
360 cacaaatgca agctcaccaa ggtcccctct cagtcccctt ccctacaccc 1000
362 tgacgccaga tgccgcacac ccaacgccac cagccatggg agtgtgctca 1050
364 ggagtcgcgg ggcagacgtg acatctgtcc agaggggggca gaatctccaa 1100
366 tagaggactg agacaacatg 1120
368 <210> SEQ ID NO: 4
369 <211> LENGTH: 172
370 <212> TYPE: PRT
371 <213> ORGANISM: Homo sapiens
373 <400> SEQUENCE: 4
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378 20 25 30
380 Ile Gln Glu Phe Lys Glu Ala Phe Asn Met Ile Asp Gln Asn Arg
381 35 40 45
383 Asp Gly Phe Ile Asp Lys Glu Asp Leu His Asp Met Leu Ala Ser
384 50 55 60
386 Leu Gly Lys Asn Pro Thr Asp Glu Tyr Leu Glu Gly Met Met Ser
387 65 70 75
389 Glu Ala Pro Gly Pro Tyr Asn Phe Thr Met Phe Leu Thr Met Phe
390 80 85 90
392 Gly Glu Lys Leu Asn Gly Thr Asp Pro Glu Asp Val Ile Arg Asn
393 95 100 105
395 Ala Phe Ala Cys Phe Asp Glu Glu Ser Ser Gly Phe Ile His Glu
396 110 115 120

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 08/04/2006  
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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; N Pos. 2298

Seq#:39; N Pos. 34

Seq#:40; Xaa Pos. 11

**VERIFICATION SUMMARY**

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L:2881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:2250

L:4157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0

L:4201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0